## SEQUENCE LISTING

<110> MARX, ACHIM

FARWICK, MIKE

HERMANN, THOMAS

SCHISCHKA, NATALIE

BATHE, BRIGITTE

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE OXYR GENE

<130> 211226US0X

<\$50> DE 10042052.4

**≪**151> 2000−08−26

**№**151> 2001-03-02

<150> US 60/279,415

<151> 2001-03-29

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1675

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (491)..(1471)

<223>

<400> 1	
gccaaccgca gggcatttac catcatggtg cgcaacgcca tgttccgcct tgtggagcta	60
thtgcttatg aaaaggaaga tcagcttagt cagatgactg aatacctgga tgaggctcct	120
gatttcggtg ctgcgatgga tgcgtacttt gatgaatatg cggatcttga taccggcccg	180
<pre> geagetegtg gaccagagtt cttcaaggta gagcacacgg gaagaatgtg ggaggtgcgt  ###  ###  ###  ###  ###  ###  #</pre>	240
daggtggtga aggatccaga aggtgataat teettegegt ttgttgeeae eattgatett	300
# datgcctctg atgatgcagg tgaggtgcgt tttggatcgc tgtcgattga ccacaactag  III	360
gggtttgcgt cgaaaagcaa gcacgcctgg tgcctgattt gagcggtttt acctatggcg	420
The state of the s	480
agttataggc atg agc aat aaa gag tac cgg ccc aca ctc gcc cag ctt Met Ser Asn Lys Glu Tyr Arg Pro Thr Leu Ala Gln Leu 1 5 10	529
cgc acc ttt gtc acc atc gca gaa tgc aag cac ttt ggt act gcc Arg Thr Phe Val Thr Ile Ala Glu Cys Lys His Phe Gly Thr Ala Ala 15 20 25	577
acc aag ctg tcc att tcg cag cca tcc ctc tcc cag gca ctt gtc gca Thr Lys Leu Ser Ile Ser Gln Pro Ser Leu Ser Gln Ala Leu Val Ala 30 35 40 45	625
tta gaa aca ggc ctg gga gtt cag ctg att gaa cgc tcc acc cgc aag Leu Glu Thr Gly Leu Gly Val Gln Leu Ile Glu Arg Ser Thr Arg Lys 50 55 60	673
gtc att gtc acc cca gcg ggc gag aag ttg ctg cca ttc gcc aaa tcc Val Ile Val Thr Pro Ala Gly Glu Lys Leu Leu Pro Phe Ala Lys Ser 65 70 75	721

* acc	c++	aac	aca	aca	gag	tct	ttc	ctc	tcc	cac	acc	aad	aac	acc	aac	769
					Glu											
					ccg Pro											817
					tca Ser 115											865
					atc Ile											913
					gcc Ala											961
gag Glu					aag Lys											1009
					gat Asp											1057
cta		_		-	gac Asp 195		-	_	_			-	_			1105
tgc					att Ile											1153
					act Thr											1201
					gtc Val											1249
					gaa Glu											1297
					acc Thr 275											1345

tcc tct tct tct cgc gcc gaa gag ttc gaa cag ttt gca ctc att ttg Ser Ser Ser Ser Arg Ala Glu Glu Phe Glu Gln Phe Ala Leu Ile Leu 290 295 300	1393
cag cgc gct ttc caa gaa gcc gtc gcg ctt gct gcc tca act ggc atc Gln Arg Ala Phe Gln Glu Ala Val Ala Leu Ala Ala Ser Thr Gly Ile 305 310 315	1441
acc ttg aag caa aat gtc gcg gta gcg cag taagtttttc tagaggtttt Thr Leu Lys Gln Asn Val Ala Val Ala Gln 320 325	1491
ccagagtcag ctacaagcaa aaagcccttt ccattgatgc acaccaacgt gagattcaag	1551
ggaaagggct ttattgattg cagaatgcct actgcattag cggcgctcca ccggaatatt	1611
tocaccactg atotggoggt aaatatgaac ggtagacagc atcattactg gcagcacgat	1671
9a1c <210> 2 <211> 327 <212> PRT	1675
<210> 2	
<pre>&lt;212&gt; PRT &lt;213&gt; Corynebacterium glutamicum &lt;400&gt; 2</pre>	
Met Ser Asn Lys Glu Tyr Arg Pro Thr Leu Ala Gln Leu Arg Thr Phe 1 5 10 15	
Val Thr Ile Ala Glu Cys Lys His Phe Gly Thr Ala Ala Thr Lys Leu 20 25 30	
Ser Ile Ser Gln Pro Ser Leu Ser Gln Ala Leu Val Ala Leu Glu Thr 35 40 45	
Gly Leu Gly Val Gln Leu Ile Glu Arg Ser Thr Arg Lys Val Ile Val 50 55 60	

Ala Ala Glu Ser Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr 4 May 1 Afa Ser Asp His Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala i alia t Glu Asp Leu Asp Leu Leu Leu Asp Asp Gly His Cys Leu His \* ... Asp Gln Ile Val Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser 

Ser Arg Ala Glu Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala 290 295 300 Phe Gln Glu Ala Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys 305 310 315 Gln Asn Val Ala Val Ala Gln 325 <210> 3 <211> 30 <212> DNA **2**13> Artificial Sequence Ų ŧŢ 220> Ţ, <del><</del>223> Synthetic DNA **₹**400> 3 gatcgagaat tcaaaggaag atcagcttag 30 ₹210> <211> 20 <212> DNA <213> Artificial Sequence <220>

20

<223>

<400> 4

Synthetic DNA

ggaaaacctc tagaaaaact